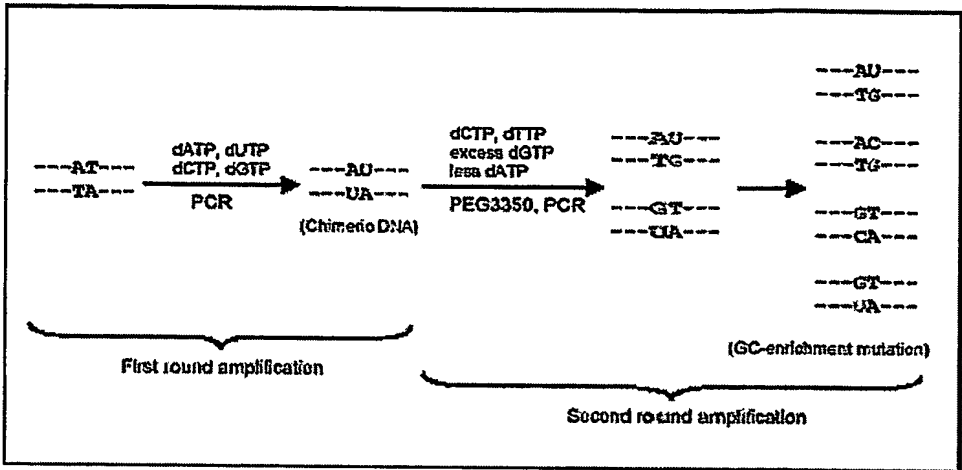


Figure 1



5

Figure 2

	34	38	41	103	105	107
AlbD	-R C I L F A A G L S G - - - G V G H S L G S V-					
Bhc	-R A V L L L N G F T G - - - V G G L S L G G V-					
Sac	-R A V L L L N G F T G - - - V A G L S L G G D-					
Lic	-R A V L L L N G F T G - - - I I G F S M G G V-					
Bac	-K A V L L L N G F T G - - - A C G L S L G G V-					
Tne	-K G V L F I N G Y T G - - - I I G F S M G G V-					
Tpc	-K A V L L I N G Y M G - - - V G G L S M G G V-					
Pcl	-Y P I I L Y N G L T G - - - L V G H S Q G G Q-					
Bsc	-A P L V L L N G F T G - - - I I A H S Q G G Q-					
Consensus	L x x x G x x G	G x S x G				
	(I)	(A)				
	(V)					

Figure 3

MDKSDLTETSRIKHGEEAFDVTL LQVKGATRCILFAAGLGGSP L RHLELLQ
TFARHGVSVVAPHFERLTSPVPTRAELLERCQRLARAQNEFCSGYASVTGV
5 GHSLGSVILL LNAGAIAMTSAGESVVFAGDRMLHRLILLAPPADFFQAPSA
LAAVNVPVHIWAGEKDSLTPPSQACFLKQALEGYTQTYLCVMEEAGHF TFM
NTLPPQVTD SHPSREAFLLDLGENIARLVTD

Figure 4

10

ATGGACAAAAGTGATCTCACGGAAACGTCTCGGATCAAACATGGGGAAGAG
GCGTTTGACGTACCTTATTGCAGGTTAAGGGGGCGACGCGCTGTATCCTT
TTTGCTGCGGGGCTGGGCGGCAGTCCGCTGCGCCATCTTGAAC TCTCCAG
ACCTTTGCCCCGCCATGGCGTTTCCGTTGTGCGGCCACACTTTGAACGGTTG
15 ACCTCACCCGTGCCCACCAGAGCTGAATTACTGGAACGCTGCCAGCGGCTT
GCGCGGGCTCAGAATGAATTTTGTAGCGGTTATGCGTCGGTTACCGGTGTT
GGCCACTCCCTGGGTAGCGTGATTTTATTGCTGAATGCCGGGGCTATAGCG
ATGACAAGCGCAGGGGAATCGGTTGTTTTCGCCGGCGACCGGATGTTGCAT
CGACTTATTTTACTGGCACCGCCCGCCGATTTTTTCCAGGCTCCGTCTGCG
20 CTGGCAGCGGTGAACGTACCTGTTACATCTGGGCAGGTGAAAAGGACAGC
CTGACGCCCCCGTCCCAGGCCTGCTTTCTTAAACAGGCACTGGAGGGTTAC
ACGCAGACTTATCTCTGTGTGATGGAAGAGGCCGGGCATTTTACCTTCATG
AATACCTTGCCTCCGCAGGTAACCGATTACATCCGTGCGGGGAGGCCTTT
CTTTTAGATTTGGGCGAAAACATAGCCCGGCTGGTGACTGAT

25